

TECH CENTER 1600/2900

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A#23 OIPE

RAW SEQUENCE LISTING

DATE: 06/03/2002

PATENT APPLICATION: US/09/126,816A

TIME: 13:00:21

Input Set : A:\98502bet.app

Output Set: N:\CRF3\06032002\I126816A.raw

3 <110> APPLICANT: VON EICHEL-STREIBER, CHRISTOPH
4 BOQUET, PATRICE
5 THELESTAM, MONICA
7 <120> TITLE OF INVENTION: METHOD OF INACTIVATION OF RAS SUBFAMILY PROTEINS AND
8 AGENTS THEREFOR
10 <130> FILE REFERENCE: 98501/254992/bet
12 <140> CURRENT APPLICATION NUMBER: 09/126,816A
C--> 13 <141> CURRENT FILING DATE: 2002-05-21
15 <150> PRIOR APPLICATION NUMBER: PCT/EP97/00426
16 <151> PRIOR FILING DATE: 1997-01-31
18 <150> PRIOR APPLICATION NUMBER: 96 101 469.3
19 <151> PRIOR FILING DATE: 1996-02-02
21 <160> NUMBER OF SEQ ID NOS: 6
23 <170> SOFTWARE: PatentIn Ver. 2.1
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 31
27 <212> TYPE: DNA
28 <213> ORGANISM: Artificial Sequence
30 <220> FEATURE:
31 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
33 <400> SEQUENCE: 1
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37 <210> SEQ ID NO: 2
38 <211> LENGTH: 29
39 <212> TYPE: DNA
40 <213> ORGANISM: Artificial Sequence
42 <220> FEATURE:
43 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
45 <400> SEQUENCE: 2
46 ttcagataat gtaggtacca agtctatag 29
49 <210> SEQ ID NO: 3
50 <211> LENGTH: 29
51 <212> TYPE: DNA
52 <213> ORGANISM: Artificial Sequence
54 <220> FEATURE:
55 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
57 <400> SEQUENCE: 3
58 ctatagactt ggtacctaca ttatctgaa 29
61 <210> SEQ ID NO: 4
62 <211> LENGTH: 28
63 <212> TYPE: DNA
64 <213> ORGANISM: Artificial Sequence
66 <220> FEATURE:

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67. <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
69 <400> SEQUENCE: 4
70   tattaacgtg ggccaatat atgtctac                               28
73 <210> SEQ ID NO: 5
74 <211> LENGTH: 25
75 <212> TYPE: PRT
76 <213> ORGANISM: Artificial Sequence
78 <220> FEATURE:
79 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
80   peptide
82 <400> SEQUENCE: 5
83   Ser Ala Leu Thr Ile Gln Leu Ile Gln Asn His Phe Val Asp Glu Tyr
84     1             5             10             15
86   Asp Pro Thr Ile Glu Asp Ser Tyr Arg
87     20             25
90 <210> SEQ ID NO: 6
91 <211> LENGTH: 2364
92 <212> TYPE: PRT
93 <213> ORGANISM: Clostridium sordellii
95 <400> SEQUENCE: 6
96   Met Asn Leu Val Asn Lys Ala Gln Leu Gln Lys Met Val Tyr Val Lys
97     1             5             10             15
99   Phe Arg Ile Gln Glu Asp Glu Tyr Val Ala Ile Leu Asn Ala Leu Glu
100    20             25             30
102  Glu Tyr His Asn Met Ser Glu Ser Ser Val Val Glu Lys Tyr Leu Lys
103    35             40             45
105  Leu Lys Asp Ile Asn Asn Leu Thr Asp Asn Tyr Leu Asn Thr Tyr Lys
106    50             55             60
108  Lys Ser Gly Arg Asn Lys Ala Leu Lys Lys Phe Lys Glu Tyr Leu Thr
109    65             70             75             80
111  Met Glu Val Leu Glu Leu Lys Asn Asn Ser Leu Thr Pro Val Glu Lys
112    85             90             95
114  Asn Leu His Phe Ile Trp Ile Gly Gly Gln Ile Asn Asp Thr Ala Ile
115    100            105            110
117  Asn Tyr Ile Asn Gln Trp Lys Asp Val Asn Ser Asp Tyr Thr Val Lys
118    115            120            125
120  Phe Val Tyr Asp Ser Asn Ala Phe Leu Ile Asn Thr Leu Lys Lys Thr
121    130            135            140
123  Ile Val Glu Ser Ala Thr Asn Asn Thr Leu Glu Ser Phe Arg Glu Asn
124    145            150            155            160
126  Leu Asn Asp Pro Glu Phe Asp Tyr Asn Lys Phe Tyr Arg Lys Arg Met
127    165            170            175
129  Glu Ile Ile Tyr Asp Lys Gln Lys His Phe Ile Asp Tyr Tyr Lys Ser
130    180            185            190
132  Gln Ile Glu Glu Asn Pro Glu Phe Ile Ile Asp Asn Ile Ile Lys Thr
133    195            200            205
135  Tyr Leu Ser Asn Glu Tyr Ser Lys Asp Leu Glu Ala Leu Asn Lys Tyr
136    210            215            220
138  Ile Glu Glu Ser Leu Asn Lys Ile Thr Ala Asn Asn Gly Asn Asp Ile

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139 225          230          235          240
141 Arg Asn Leu Glu Lys Phe Ala Asp Glu Asp Leu Val Arg Leu Tyr Asn
142          245          250          255
144 Gln Glu Leu Val Glu Arg Trp Asn Leu Ala Ala Ala Ser Asp Ile Leu
145          260          265          270
147 Arg Ile Ser Met Leu Lys Glu Asp Gly Gly Val Tyr Leu Asp Val Asp
148          275          280          285
150 Ile Leu Pro Gly Ile Gln Pro Asp Leu Phe Lys Ser Ile Asn Lys Pro
151          290          295          300
153 Asp Ser Ile Thr Asn Thr Ser Trp Glu Met Ile Lys Leu Glu Ala Ile
154 305          310          315          320
156 Met Lys Tyr Lys Glu Tyr Ile Pro Gly Tyr Thr Ser Lys Asn Phe Asp
157          325          330          335
159 Met Leu Asp Glu Glu Val Gln Arg Ser Phe Glu Ser Ala Leu Ser Ser
160          340          345          350
162 Lys Ser Asp Lys Ser Glu Ile Phe Leu Pro Leu Asp Asp Ile Lys Val
163          355          360          365
165 Ser Pro Leu Glu Val Lys Ile Ala Phe Ala Asn Asn Ser Val Ile Asn
166          370          375          380
168 Gln Ala Leu Ile Ser Leu Lys Asp Ser Tyr Cys Ser Asp Leu Val Ile
169 385          390          395          400
171 Asn Gln Ile Lys Asn Arg Tyr Lys Ile Leu Asn Asp Asn Leu Asn Pro
172          405          410          415
174 Ser Ile Asn Glu Gly Thr Asp Phe Asn Thr Thr Met Lys Ile Phe Ser
175          420          425          430
177 Asp Lys Leu Ala Ser Ile Ser Asn Glu Asp Asn Met Met Phe Met Ile
178          435          440          445
180 Lys Ile Thr Asn Tyr Leu Lys Val Gly Phe Ala Pro Asp Val Arg Ser
181          450          455          460
183 Thr Ile Asn Leu Ser Gly Pro Gly Val Tyr Thr Gly Ala Tyr Gln Asp
184 465          470          475          480
186 Leu Leu Met Phe Lys Asp Asn Ser Thr Asn Ile His Leu Leu Glu Pro
187          485          490          495
189 Glu Leu Arg Asn Phe Glu Phe Pro Lys Thr Lys Ile Ser Gln Leu Thr
190          500          505          510
192 Glu Gln Glu Ile Thr Ser Leu Trp Ser Phe Asn Gln Ala Arg Ala Lys
193          515          520          525
195 Ser Gln Phe Glu Glu Tyr Lys Lys Gly Tyr Phe Glu Gly Ala Leu Gly
196          530          535          540
198 Glu Asp Asp Asn Leu Asp Phe Ala Gln Asn Thr Val Leu Asp Lys Asp
199 545          550          555          560
201 Tyr Val Ser Lys Lys Ile Leu Ser Ser Met Lys Thr Arg Asn Lys Glu
202          565          570          575
204 Tyr Ile His Tyr Ile Val Gln Leu Gln Gly Asp Lys Ile Ser Tyr Glu
205          580          585          590
207 Ala Ser Cys Asn Leu Phe Ser Lys Asp Pro Tyr Ser Ser Ile Leu Tyr
208          595          600          605
210 Gln Lys Asn Ile Glu Gly Ser Glu Thr Ala Tyr Tyr Tyr Val Ala
211          610          615          620

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213 Asp Ala Glu Ile Lys Glu Ile Asp Lys Tyr Arg Ile Pro Tyr Gln Ile
214 625 630 635 640
216 Ser Asn Lys Arg Asn Ile Lys Leu Thr Phe Ile Gly His Gly Lys Ser
217 645 650 655
219 Glu Phe Asn Thr Asp Thr Phe Ala Asn Leu Asp Val Asp Ser Leu Ser
220 660 665 670
222 Ser Glu Ile Glu Thr Ile Leu Asn Leu Ala Lys Ala Asp Ile Ser Pro
223 675 680 685
225 Lys Tyr Ile Glu Ile Asn Leu Leu Gly Cys Asn Met Phe Ser Tyr Ser
226 690 695 700
228 Ile Tyr Ala Glu Glu Thr Tyr Pro Gly Lys Leu Leu Lys Ile Lys
229 705 710 715 720
231 Asp Arg Val Ser Glu Leu Met Pro Ser Ile Ser Gln Asp Ser Ile Thr
232 725 730 735
234 Val Ser Ala Asn Gln Tyr Glu Val Arg Ile Asn Glu Glu Gly Lys Arg
235 740 745 750
237 Glu Ile Leu Asp His Ser Gly Lys Trp Ile Asn Lys Glu Glu Ser Ile
238 755 760 765
240 Ile Lys Asp Ile Ser Ser Lys Glu Tyr Ile Ser Phe Asn Pro Lys Glu
241 770 775 780
243 Asn Lys Ile Ile Val Lys Ser Lys Tyr Leu His Glu Leu Ser Thr Leu
244 785 790 795 800
246 Leu Gln Glu Ile Arg Asn Asn Ala Asn Ser Ser Asp Ile Asp Leu Glu
247 805 810 815
249 Lys Lys Val Met Leu Thr Glu Cys Glu Ile Asn Val Ala Ser Asn Ile
250 820 825 830
252 Asp Arg Gln Ile Val Glu Gly Arg Ile Glu Glu Ala Lys Asn Leu Thr
253 835 840 845
255 Ser Asp Ser Ile Asn Tyr Ile Lys Asn Glu Phe Lys Leu Ile Glu Ser
256 850 855 860
258 Ile Ser Asp Ser Leu Tyr Asp Leu Lys His Gln Asn Gly Leu Asp Asp
259 865 870 875 880
261 Ser His Phe Ile Ser Phe Glu Asp Ile Ser Lys Thr Glu Asn Gly Phe
262 885 890 895
264 Arg Ile Arg Phe Ile Asn Lys Glu Thr Gly Asn Ser Ile Phe Ile Glu
265 900 905 910
267 Thr Glu Lys Glu Ile Phe Ser Glu Tyr Ala Thr His Ile Ser Lys Glu
268 915 920 925
270 Ile Ser Asn Ile Lys Asp Thr Ile Phe Asp Asn Val Asn Gly Lys Leu
271 930 935 940
273 Val Lys Lys Val Asn Leu Asp Ala Ala His Glu Val Asn Thr Leu Asn
274 945 950 955 960
276 Ser Ala Phe Phe Ile Gln Ser Leu Ile Glu Tyr Asn Thr Thr Lys Glu
277 965 970 975
279 Ser Leu Ser Asn Leu Ser Val Ala Met Lys Val Gln Val Tyr Ala Gln
280 980 985 990
282 Leu Phe Ser Thr Gly Leu Asn Thr Ile Thr Asp Ala Ser Lys Val Val
283 995 1000 1005
285 Glu Leu Val Ser Thr Ala Leu Asp Glu Thr Ile Asp Leu Leu Pro Thr

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286      1010      1015      1020
288 Leu Ser Glu Gly Leu Pro Ile Ile Ala Thr Ile Ile Asp Gly Val Ser
289 1025      1030      1035      1040
291 Leu Gly Ala Ala Ile Lys Glu Leu Ser Glu Thr Asn Asp Pro Leu Leu
292      1045      1050      1055
294 Arg Gln Glu Ile Glu Ala Lys Ile Gly Ile Met Ala Val Asn Leu Thr
295      1060      1065      1070
297 Ala Ala Ser Thr Ala Ile Val Thr Ser Ala Leu Gly Ile Ala Ser Gly
298      1075      1080      1085
300 Phe Ser Ile Leu Leu Val Pro Leu Ala Gly Ile Ser Ala Gly Ile Pro
301      1090      1095      1100
303 Ser Leu Val Asn Asn Glu Leu Ile Leu Gln Asp Lys Ala Thr Lys Val
304 1105      1110      1115      1120
306 Ile Asp Tyr Phe Lys His Ile Ser Leu Ala Glu Thr Glu Gly Ala Phe
307      1125      1130      1135
309 Thr Leu Leu Asp Asp Lys Ile Ile Met Pro Gln Asp Asp Leu Val Leu
310      1140      1145      1150
312 Ser Glu Ile Asp Phe Asn Asn Asn Ser Ile Thr Leu Gly Lys Cys Glu
313      1155      1160      1165
315 Ile Trp Arg Ala Glu Gly Gly Ser Gly His Thr Leu Thr Asp Asp Ile
316      1170      1175      1180
318 Asp His Phe Phe Ser Ser Pro Ser Ile Thr Tyr Arg Lys Pro Trp Leu
319 1185      1190      1195      1200
321 Ser Ile Tyr Asp Val Leu Asn Ile Lys Lys Glu Lys Ile Asp Phe Ser
322      1205      1210      1215
324 Lys Asp Leu Met Val Leu Pro Asn Ala Pro Asn Arg Val Phe Gly Tyr
325      1220      1225      1230
327 Glu Met Gly Trp Thr Pro Gly Phe Arg Ser Leu Asp Asn Asp Gly Thr
328      1235      1240      1245
330 Lys Leu Leu Asp Arg Ile Arg Asp His Tyr Glu Gly Gln Phe Tyr Trp
331      1250      1255      1260
333 Arg Tyr Phe Ala Phe Ile Ala Asp Ala Leu Ile Thr Lys Leu Lys Pro
334 1265      1270      1275      1280
336 Arg Tyr Glu Asp Thr Asn Val Arg Ile Asn Leu Asp Gly Asn Thr Arg
337      1285      1290      1295
339 Ser Phe Ile Val Pro Val Ile Thr Thr Glu Gln Ile Arg Lys Asn Leu
340      1300      1305      1310
342 Ser Tyr Ser Phe Tyr Gly Ser Gly Gly Ser Tyr Ser Leu Ser Leu Ser
343      1315      1320      1325
345 Pro Tyr Asn Met Asn Ile Asp Leu Asn Leu Val Glu Asn Asp Thr Trp
346      1330      1335      1340
348 Val Ile Asp Val Asp Asn Val Val Lys Asn Ile Thr Ile Glu Ser Asp
349 1345      1350      1355      1360
351 Glu Ile Gln Lys Gly Glu Leu Ile Glu Asn Ile Leu Ser Lys Leu Asn
352      1365      1370      1375
354 Ile Glu Asp Asn Lys Ile Ile Leu Asn Asn His Thr Ile Asn Phe Tyr
355      1380      1385      1390
357 Gly Asp Ile Asn Glu Ser Asn Arg Phe Ile Ser Leu Thr Phe Ser Ile
358      1395      1400      1405

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VERIFICATION SUMMARY

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L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date